

Figure 25 continued :

Sbjct: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
YKIADPICTYVFSLLVAFTTFRIIWDTVVILEGVPSHLNVDYIKEALMKIEDVYSVEDL

Sbjct: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360

108P5: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLNTFGMYRCTIQLQSYRQEVDR 420
NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLNTFGMYRCTIQLQSYRQEVDR

Sbjct: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLNTFGMYRCTIQLQSYRQEVDR 420

108P5: 421 CANCQSSSP 429
CANCQSSSP

Sbjct: 421 CANCQSSSP 429

C-Alignment of 108P5H8 (SEQ. ID. No.: 2580) with the rat zinc transporter ZNT-4, i.e. gi 8134837 (SEQ. ID. No.: 2581).

Identities = 387/430 (90%), Positives = 407/430 (94%), Gaps = 3/430 (0%)

108P5: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
MAG GAWKRLKS+LRKDDAPLFLNDTSAFDF DE DEGLSRFNKLRVVVADD SEAPER

Sbjct: 1 MAGPGAWKRLKSLLRKDDAPLFLNDTSAFDFLDEVSEGLSRFNKLRVVVADDSEAPER 60

108P5: 61 PVNGAHP TLQADDDSLDQDLPLTNSQLSLKVDSCDNC SKQREILKQKVKARLTIAAVL 120
PVNGAHP LQADDDSLDQ+LPLTNSQLSLK+D CDNCSK+RE+LKQKVK RTIAAVL

Sbjct: 61 PVNGAHPALQADDDSLDQELPLTNSQLSLKMPDCDNC SKRRELLKQKVKTRLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAIILTLLALWLSSKSPTKRFTFGFHRLE 180
YLLFMIGELVGGY+ANS LAIMTDALHMLTDL SAIILTLLALWLSSKSPT+RFTFGFHRLE

Sbjct: 121 YLLFMIGELVGGYMANSLAIMTDALHMLTDL SAIILTLLALWLSSKSPTRRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQ-- 238
VLSAMISV+LVY+LMGFLLYE+QRTIHMNYEINGD+MLITAAGVAVNVIMGFLLNQ

Sbjct: 181 VLSAMISVMLVYVLMGFLLYEAMQRTIHMNYEINGDVMLITAAGVAVNVIMGFLLNQSG 240

108P5: 239 SGHRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 298
H H+HSHSLPSNSP+ S +HGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK

Sbjct: 241 HHHSHSHSHSLPSNSPSMVSS-GHSHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 299

108P5: 299 PEYKIADPICTYVFSLLVAFTTFRIIWDTVVILEGVPSHLNVDYIKEALMKIEDVYSVE 358
PEYKIADPICTY+FSLLVAFTT RIIWDTVVILEGVPSHLNVDYIKE+LMKIEDVYSVE

Sbjct: 300 PEYKIADPICTYIFSLVAFTTLRIIWDTVVILEGVPSHLNVDYIKESLMKIEDVYSVE 359

108P5: 359 DLNIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLNTFGMYRCTIQLQSYRQEVDR 418
DLNIWSLTSGK+TAIVH+QLIPGSSSKWEEVQSKA HLLNTFGMY+CT+QLQSYRQE

Sbjct: 360 DLNIWSLTSGKATAIVHMLIPGSSSKWEEVQSKAKHLLNTFGMYKCTVQLQSYRQEAT 419

108P5: 419 RTCANCQSSS 428
RTCANCQSSS

Sbjct: 420 RTCANCQSSS 429